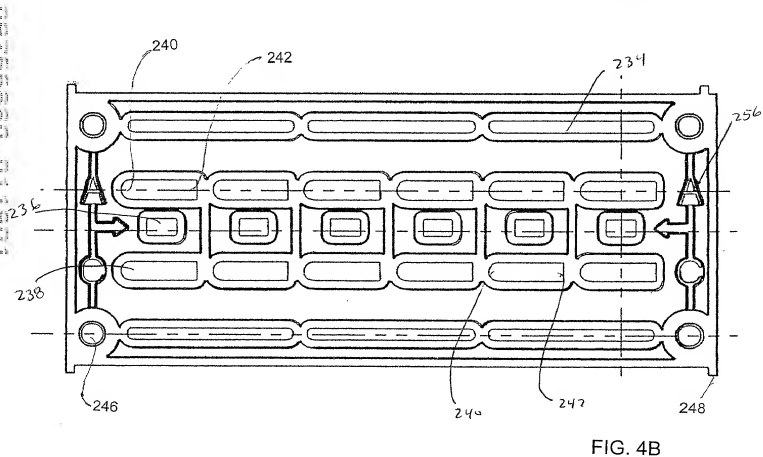
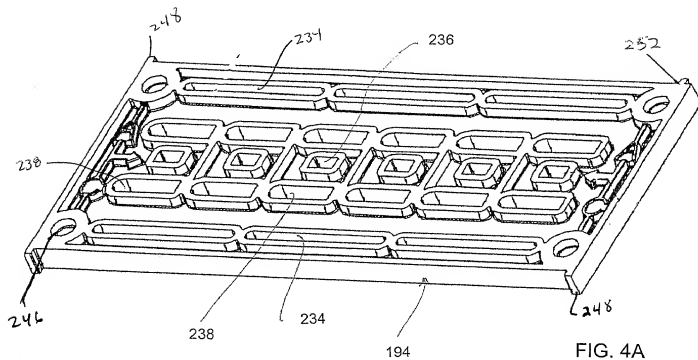


FIG. 2



FIG. 3





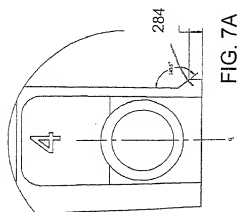


FIG. 7A



FIG. 7E

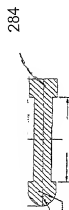


FIG. 7F

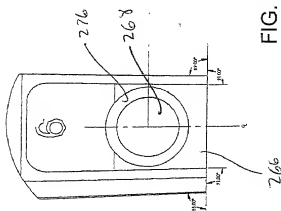


FIG. 7B

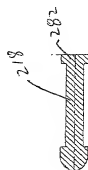


FIG. 7G

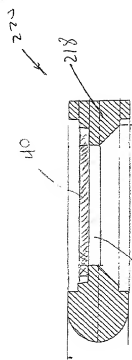


FIG. 7C

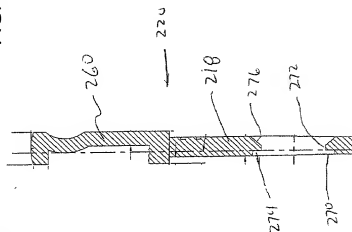
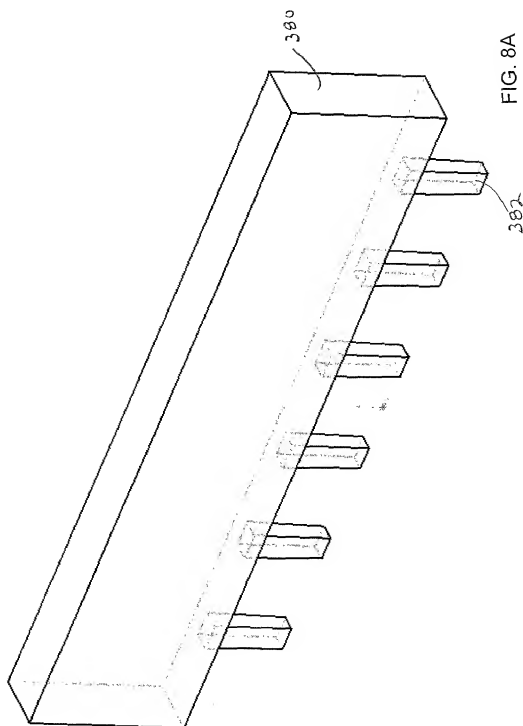


FIG. 7D



106370-00009240

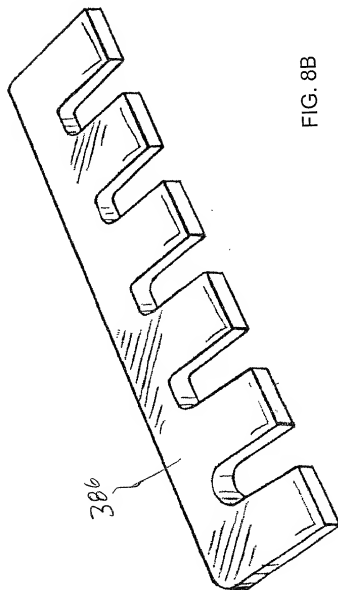
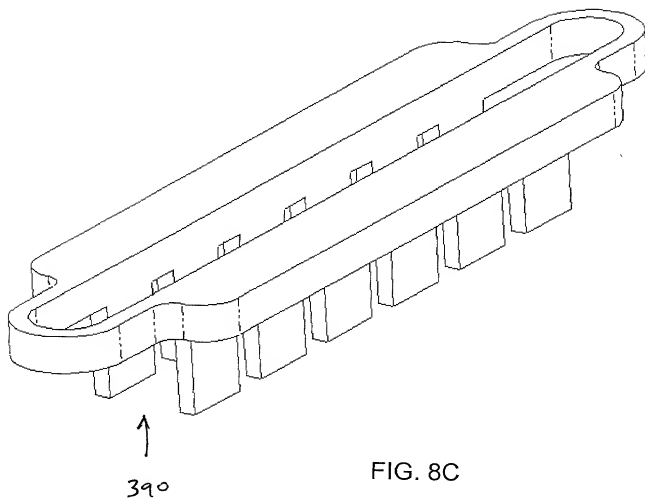


FIG. 8B

105413-00002450





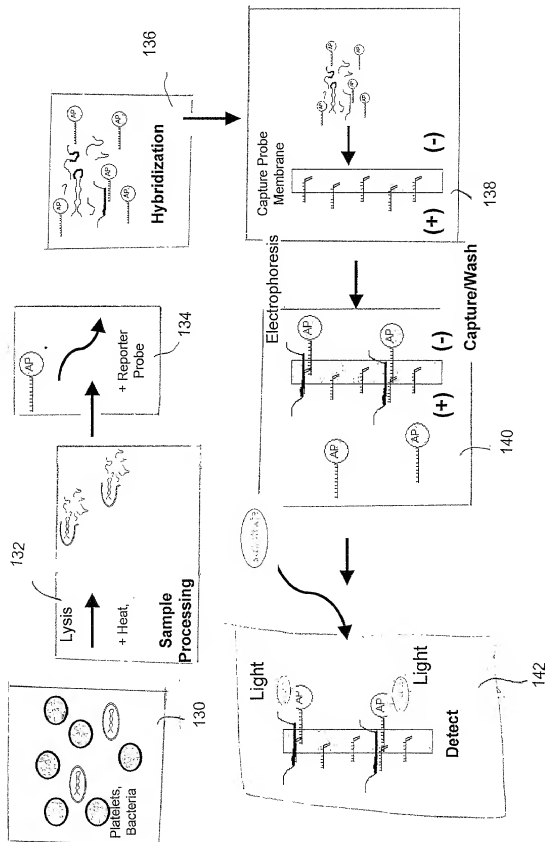


FIG. 9A

106110-0099/60

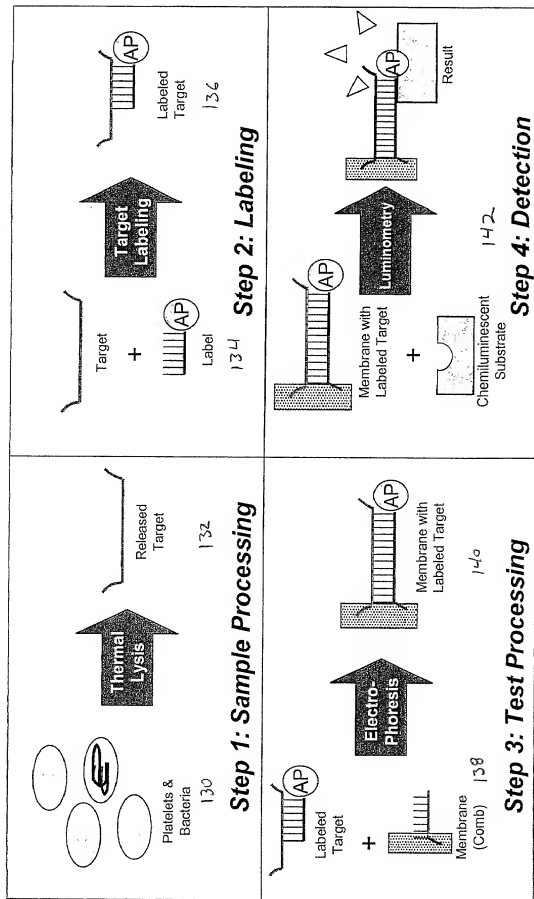


FIG. 9B

# Staphylococcus species (\* all unfinished)

staph\_epi : CATTAAC CATCTCAGGTCCTGACGGAGCAGC CATTAACGCAATCTCAATA : 198  
 Staph\_prob : -----CACTCAGGTCCTGACGGAGCAGC ----- : 26  
 saureus\_co : CATTAAC CATCTCAGGTCCTGACGGAGCAGC CATTAACGCAATCTCAATA : 200  
 catgaaccCATCTCAGGTCCTGACGGAGCAGCattagtggtgc tcata

# Streptococcus species (\* all unfinished)

Streppyo\_ : CTGCGGCTCAAGTCGGGTCAGGGGAGGAATCCAGCAGC CTAAGGC : 220  
 Streppneum : GTTCGCGGCTCAAGTCGGGTCAGGGGAGGAATCCAGCAGC CTAAGGC : 92  
 strep\_targ : -----ATCGGTCAGGGGAGGAATCCAGCAGC ----- : 26  
 Strep\_Equi : CTGCGGCTCAAGTCGGGTCAGGGGAGGAATCCAGCAGC CTAAGGC : 135  
 strepmutan : GCTTCGCTCAAGTCGGGTCAGGGGAGGAATCCAGCAGC CTAAGGC : 221  
 t tgcgtgaag GGGTCAGGGGAGGAATCCAGCAGCc taagcg

# Enterobacteriaceae, Pseudomonas aeruginosa, Bacillus cereus

\* klebpneum : GGTAACTCTACTTCTTTCTCAGGTCGGAGGAAGCAGC -GAGGACGAGGTCTCA : 115  
 \* Stypthimurw : GGTAACTCTACTTCTTTCTCAGGTCGGAGGAAGCAGC -GAGGACGAGGTCTCA : 84  
 ecoli\_comp : GGTAACTCTACTTCTTTCTCAGGTCGGAGGAAGCAGC -GAGGACGAGGTCTCA : 84  
 Ecoli\_prob : -----ACAGCTCAGGTCGGAGGAAGCAGC ----- : 26  
 pseudauerug : GGTAACTCTACTTCTTTCTCAGGTCGGAGGAAGCAGC -GAGGACGAGGTCTCA : 84  
 Bacillus\_c : GGTAACTCTACTTCTTTCTCAGGTCGGAGGAAGCAGC -GAGGACGAGGTCTCA : 194  
 cgcacgc c gt acC gGTCAGGTCGGAGGAAGCAGC a gc g gtgt

\* unfinished sequence from genome centers

FIG. 9C

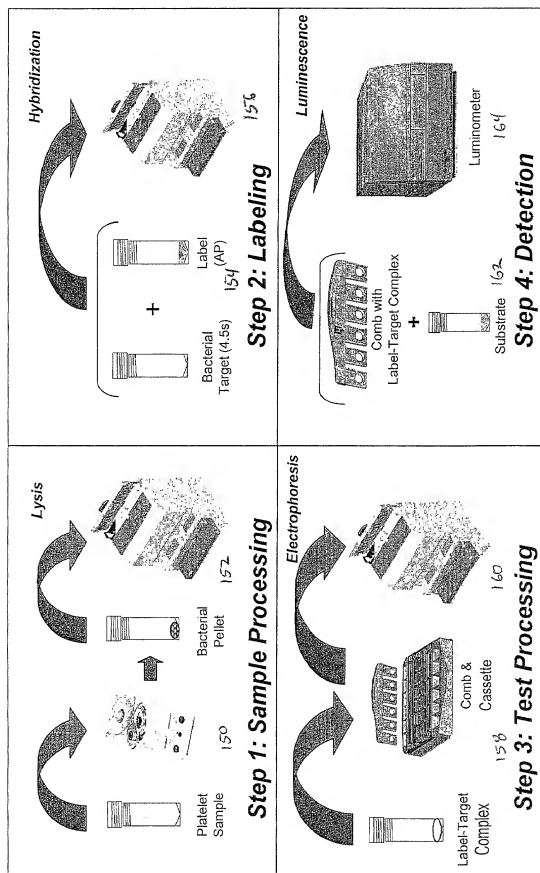
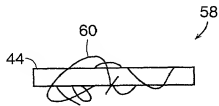
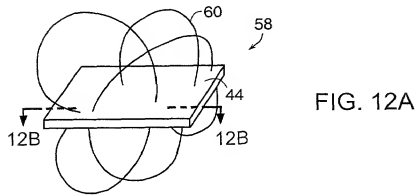
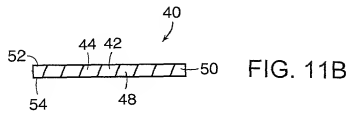
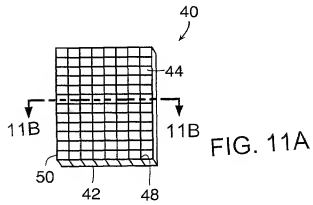


FIG. 10



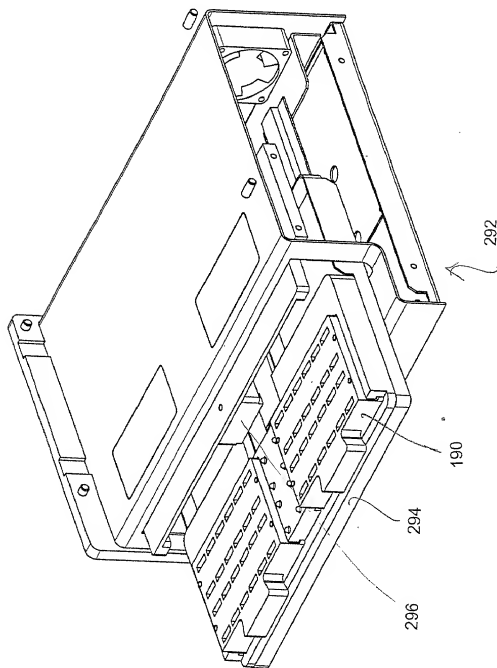


FIG. 13

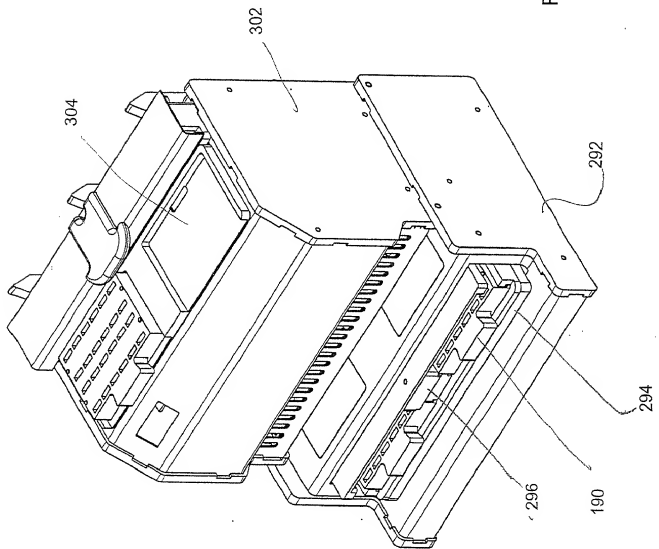
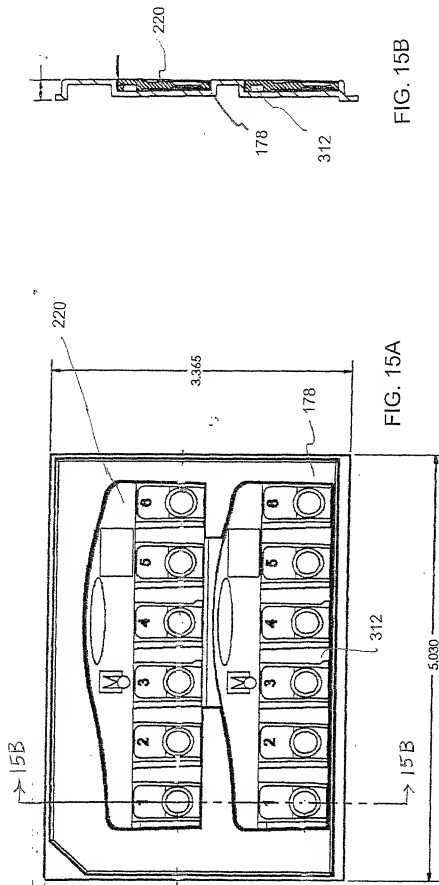


FIG. 14





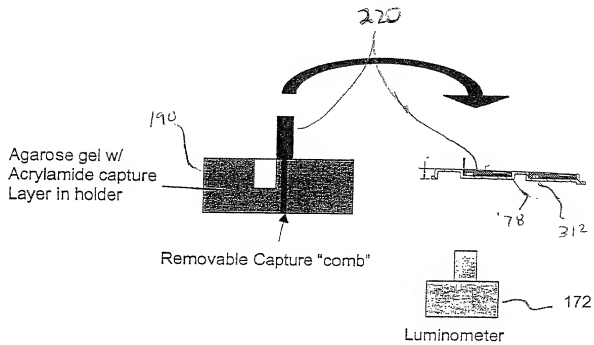


FIG. 16

105110-09999760

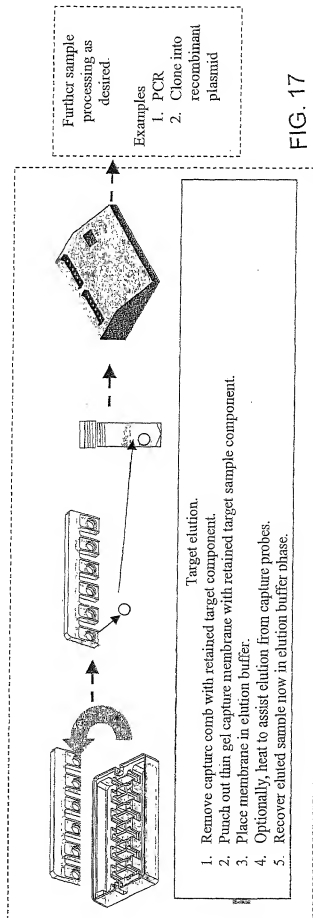
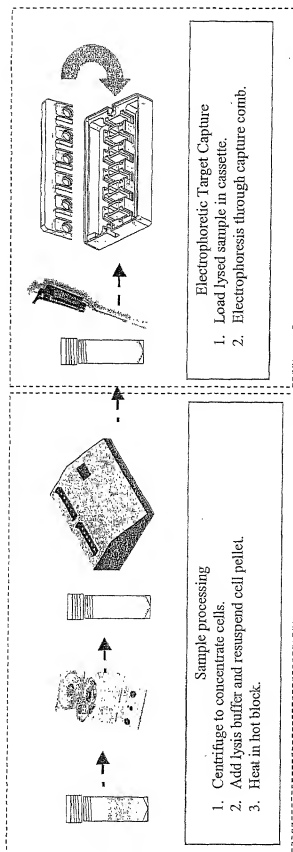
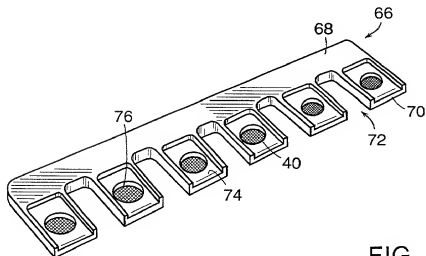
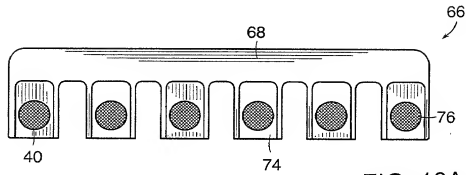


FIG. 17



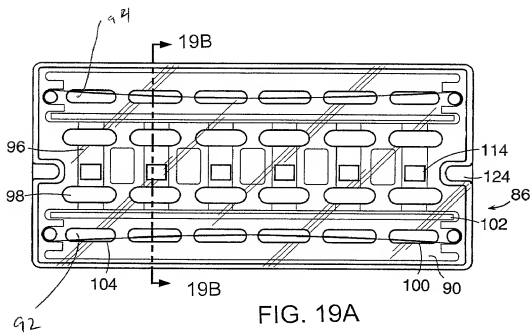


FIG. 19A

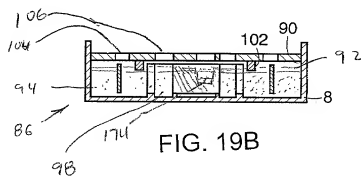


FIG. 19B

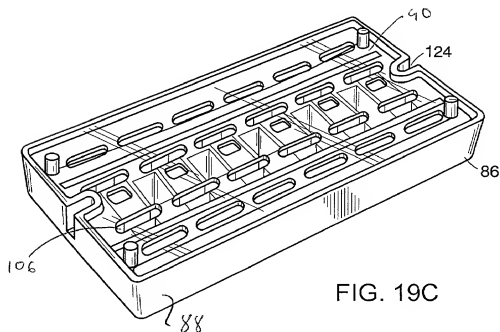


FIG. 19C

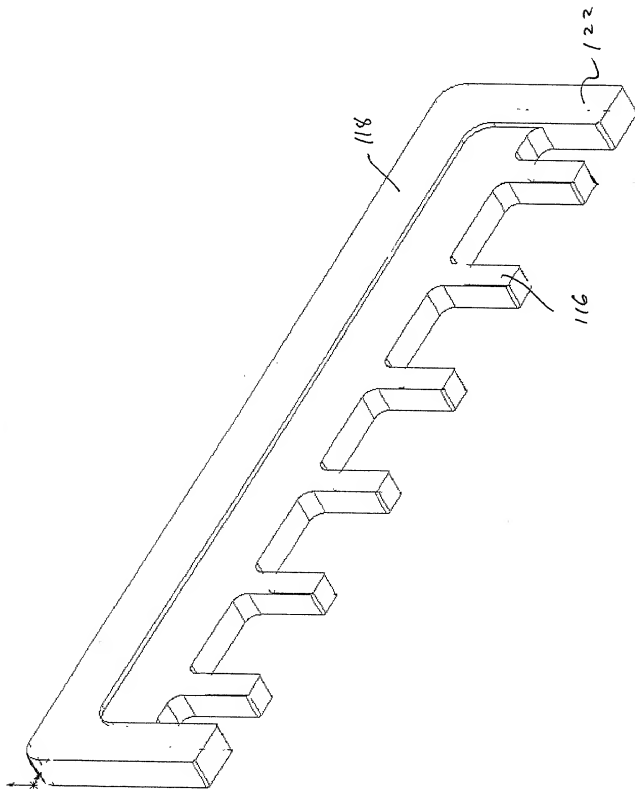


FIG. 20

10617101 00099260

FIG. 21A

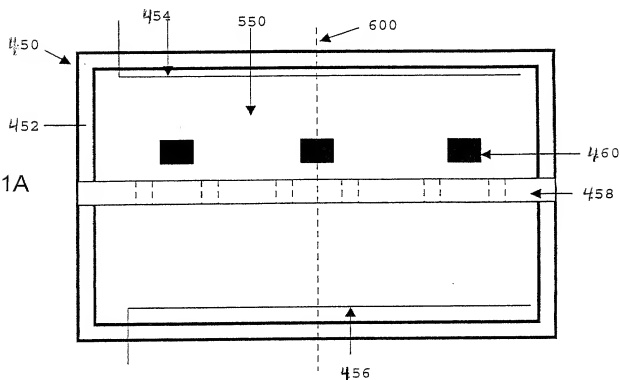


FIG. 21B

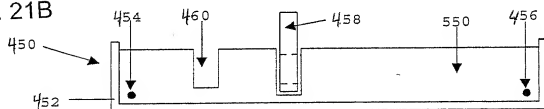
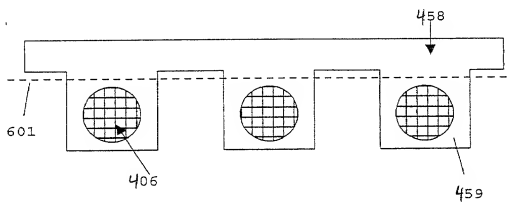


FIG. 21C



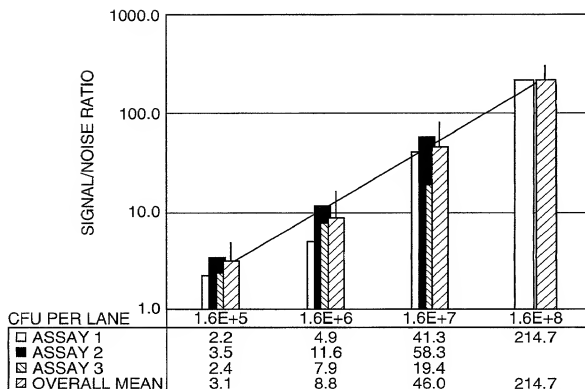
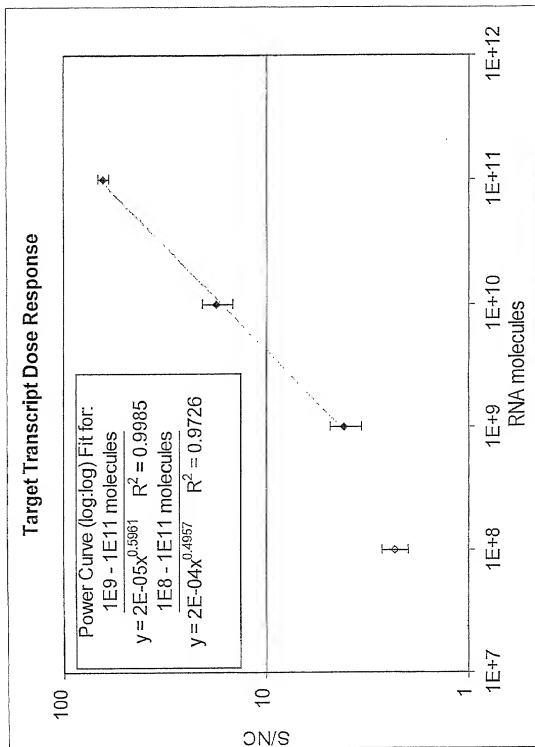


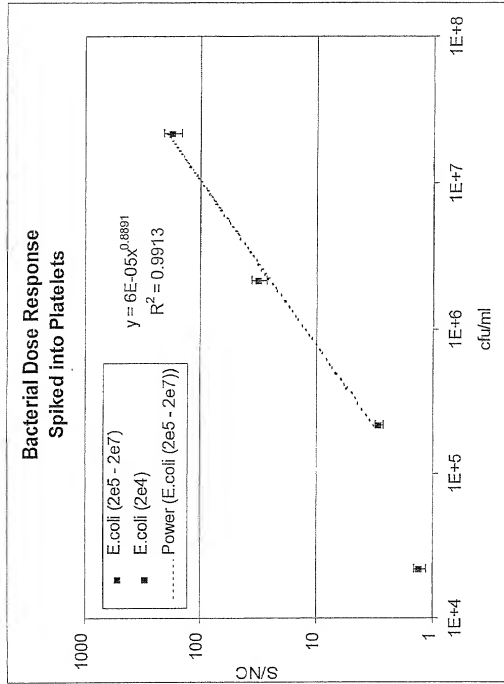
FIG. 22





- S/N from target transcripts spiked into assay after centrifugation step (mean  $\pm$  s.e. ( $n=13$ ))
- Copy# of 4.5S in *E. coli*  $\sim 1,000$ /ctu

FIG. 23



- S/N from *E.coli* (n=8) spiked into negative platelets, then processed according to the assay scheme (mean  $\pm$  s.e.).

FIG. 24

Assay Time	
Sample Processing	Assay
Target Enrichment	Probe Hybridization
Rinse	Electrophoretic Capture
Lysis	Wash
Cool	Detection
	11min
	20min
	5min
	10min

12 - 15 minutes 45 - 50 minutes

Centrifuge samples x 1min  
 Uncap, pour off liquid - BIOHAZARD  
 Pipet Rinse Buffer  
 Vortex to resuspend  
 Centrifuge samples x 1min  
 Uncap, pour off liquid - BIOHAZARD  
 Pipet Lysis Buffer  
 Vortex to resuspend  
 Obtain NC and PC tubes  
 Place NC, PC and sample tubes in heater  
 Incubate through heat-cool cycle  
 5min at >100C => 2min to 45C

Pipet Hybridization Buffer  
 Mix by inversion several times  
 Incubate 10min at 45C.

Pipet 50ul from each tube into cassette  
 Electrophorese for 20min

Move comb to Wash Buffer 1  
 Move comb to electroph wash slot  
 Electrophorese for 3min  
 Move comb to Conditioning Buffer  
 Dry comb  
 Pipet Substrate  
 Load Reader  
 Results Displayed

FIG. 25